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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Title: Perfect score: OM nucleic - nucleic search, using sw model Searched: Scoring table: Sequence: Run on: US-09-675-650-2 278 1 caggaagcacaaaa GenEmbl:*
1: gb_ba:*
2: gb_htg: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 February 1, 2004, 08:17:56; Search time 1513 Seconds (without alignments) 7516.772 Million cell updates/sec 2888711 segs, 20454813386 residues caggaagcacaaaaggaagc.....ggcttcacaagacatgcaac 278 gb ba: *
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Pred. No. is the number of results predicted by chance to have a

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                    Skeiky,Y.A., Xu,J., Cheever,M.A. and Reed,S.G. Compositions and methods for wtl specific immunotherapy Patent: Wo 0125273-A 345 12-APR-2001; CORIXA CORPORATION (US)
                                                                                          Homo sapiens (human)
                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Sequence 47
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Kalos,M.D., Fanger,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
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Location/Qualifiers

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Sequence 471 from Patent
AX106690
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CORPORATION (US)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
189 c 169 g 25
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/mol_type="genomic DNA"
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189 c 169 g 25
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Pred. No. 2e-68;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 471 from Patent
AX140981
AX140981.1 GI:14281078
Xu,J.,
                                                                                    Sequence 471 from Paten
AX200841
AX200841.1 GI:15390744
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                                                Homo sapiens
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                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Dillon, D.C., Mitcham, J.L.,
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
189 c 169 g 25
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Day,C.H.,
                                       Euteleostomi;
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Sequence 471 from Patent
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                                                                                                                                                                                                                                  Xu,J. Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedwick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A.
                                                                                                                                                                                 cancer
Patent: WO 0173032-A 471 04-OCT-2001;
CORIXA CORPORATION (US)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 2e-68;
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Pred. No. 2e-68;
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Best Local :
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PN JP 2001522240-A/3
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/:
C1201/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
FH Key Table (1998)
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277; Conserv
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JP 2001522240-A/3.
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BD082484
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                               AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGAAAAC
                                                                                  AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 278
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                 AACGGGATTACAGATTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                                                      AACGGGATTACAGATTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAGGAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                             JP 200152240-A/3
13-NOV-2001
09-APR-1998 JP 1998542194
10-APR-1997 US 60/041836
MARION J G BUSSEMAKERS
C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18,
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                                                                     GI:22628094
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99.6%;
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Pred. No. 2e-68;
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PAT 27-AUG-2002

Indels

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Gaps

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241

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RESULT 10
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BD082482
LOCUS
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ACCESSION
VERSION
KEYWORDS
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KEYWORDS
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Best Local Similarity
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ORGANISM
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                                                                                                                                                                                                           181 AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC
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Patent: JP 200152240-A 2
DIAGNOCURE INC
PN JP 2001522240-A/2
PD 13-NOV-2001
PF 09-APR-1998 JP 19985-
PR 10-APR-1997 US 60,
PI MARION J G BUSSEMAKEE
PC C12N15/00,C12N15/12,(
C1201/68,
PC G01N33/577,A61K39/39)
CC Strandedness: Double
CC Topology: Linear;
FH Key
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BD082483
                                             BD082482 2037 PCA3, PCA3 genes, and methods BD082482
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                      BD082482.1 GI:22628092
JP 2001522240-A/1.
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09-APR-1998 JP 1998542194
10-APR-1997 US 60/041836
MARION J G BUSSEMAKERS
C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18,
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Strandedness: Double;
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/mol_type="genomic DNA"
/db_xref="taxon:10509"
389 c 369 g 539 1
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99.6%;
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Pred. No. 2.2e-68;
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13-NOV-2001;
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JOURNAL
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Best Local
Query Match
Best Local Similarity
                                                                                                                                                                    ORGANISM
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PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C0
C12Q1/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Topology: Linear; FH Key
FT CDS 13/93-531.
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                                                                                                                                                                                                                     Sequence
AR261037
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                                                                         Negative pressure control apparatus for Patent: US 6321716-A 469 27-NOV-2001; Cocation/Qualifiers
                                                                                                                             1 (bases 1 to 2229)
Mashiki, Z. and Harada, J.
                                                                                                                                                                 Unknown
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1 (bases 1 to 2037)
                                                                                                                                                      Unclassified
                                                                                                                                                                                  Unknown
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10-APR-1997 US 60/041836
MARION J G BUSSEMAKERS
C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18,
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/mol_type="genomic DNA"
/db_xref="taxon:10509"
426 c 406 g 575 t
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                                                 /organism="unknown"
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Pred. No. 2.2e-68;
0; Mismatches 0
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Pred.
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 266; DB 6;
No. 2.2e-68;
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis o
                                                                                                                                                                                                                                                                                                                                         Patent: US 6512094-A 469 28-JAN-2003;
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Sequence 343 from Patent
AX106205
AX106205.1 GI:13921894
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AX106688
AX106688.1 GI:13922353
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                      Homo sapiens (human)
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/mol_type="genomic DNA"
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           /organism="Homo sapiens"
/mol_type="genomic DNA"
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Query Match Best Local	Query Match 95.7%; Score 266; DB 6; Length 2229; Best Local Similarity 99.6%; Pred. No. 2.2e-68;
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γQ	61 TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAAATG 120
망	1557 TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG 1498
У	121 AATTGATGTGTTCCTTAAAGGATGGGCAGGAAAACAGATCCTGTTGTGGATATTTATT
Db	1497 AATTGATGTGTTCCTTAAAGGATGGGCAGGAAAACAGATCCTGTTGTGGATATTTATT
Qy	181 AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC 240
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-09-352-616A-313
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ty 95. ervative ervative	US-09-439-313-471/c US-09-439-313-471/c Sequence 471, Application US/0943931 Patent No. 6329505 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Mitcham, Jennifer L. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan Louise APPLICANT: Harlocker, Susan Louise APPLICANT: Reed, Steven G. APPLICANT: Reed, Steven G. APPLICANT: Renger, Gary APPLICANT: Retter, Mark APPLICANT: Retter, Mark APPLICANT: Day, Craig TITLE OF INVENTION: COMPOSITIONS AN TITLE OF INVENTION: DIAGNOSIS OF INTERION NUMBER: US/09/4 CURRENT APPLICATION NUMBER: US/09/4 CURRENT FILING DATE: 1999-11-12 NUMBER OF SEQ ID NOS: 575 SOFTWARE: FastSEQ for Windows Versi SEQ ID NO 471 LENGTH: 812 TYPE: DNA ORGANISM: Homo sapiens	9641 2085 2085 2085 2087 152331 1830121 1830121 1830121 1932 1922 1922 1952 1952 3460 4074
77 3G 3G 3G 4G	ss/o C. C. fer an an ocsi (C9 100SI	4224504 43011424242
95.7%; Score 266; DB 4; Length 812; caggaagcacaaaaggaagcacagaagcacacagagaaccagagaaaaaa	3 METHODS FOR THERAPY PROSTATE CANCER 139,313 LON 3.0	US-09-625-972-22 US-08-668-128B-7 US-08-955-445-7 US-09-220-132-79 US-09-128-155-16 US-09-128-155-17 US-08-945-528D-1 US-09-557-884-1 US-09-643-990A-1 US-09-07-532A-1113 US-08-960-780-3 US-08-471-033-19 US-08-471-033-19 US-08-471-044-19
812; 8 1; Gaps 1 GCCGCCATCTTGGG 60	DUA	Sequence 22, Appli Sequence 7, Appli Sequence 7, Appli Sequence 19, Appli Sequence 16, Appli Sequence 17, Appli Sequence 11, Appli Sequence 11, Appli Sequence 1113, Appli Sequence 33, Appl Sequence 34, Appli Sequence 1, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli

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241 AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 278

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-471
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Best Local Similarity 99.6%;
Matches 277; Conservative
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SEQ ID NO 471
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Nitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427CB
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
RUMBER OF SEQ ID NOS: 472
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Solk, John
APPLICANT: Day, Craig
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
                                                                                                                                                                                                                                APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Harlocker, Susan Lou
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                                                                                                                                                                                                                                                                                                                 INFORMATION:
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Retter, Mark
Solk, John
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Reed, Steven G.
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
INUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
TYPE: DNA
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; Sequence 469, Application US/09352616A
; Patent No. 6395278
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APPLICANT: Dillon, Dav
APPLICANT: Harlocker,
APPLICANT: Jiang, Yuqu
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Matches 277; Conserv
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
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 AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAAC
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Xu, Jiangchun
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Pred. No. 1.6e-79;
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Pred. No. 1.6e-79;
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APPLICANT: Day, Craig
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 470
LENGTH: 2426
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-470
                                                                                                                                             RESULT 6
US-09-352-616A-470/c
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US-09-439-313-470/c
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GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
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Best Local Similarity
Matches 277; Conserv
                                                                                                                   Sequence 470, Application Patent No. 6395278
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APPLICANT:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Fanger, Gary
Retter, Mark
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Reed, Steven G.
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Pred. No. 1.6e-79;
0; Mismatches 0
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; TITLE OF INVENTION: OF PROSTATE CANCER AND MET; FILE REFERENCE: 210121.427C8; CURRENT APPLICATION NUMBER: US/09/352,616A; CURRENT FILING DATE: 1999-07-13; NUMBER OF SEQ ID NOS: 472; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 470; SEQ ID NO 470; LENGTH: 2426; TYPE: DNA GRANISM: Homo sapiens
US-09-352-616A-470
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                                                                                                            ; ORGANISM: Homo sapiens US-09-439-313-468
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                                                                                                                                        NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
                                         Query Match
Best Local Similarity
Matches 277; Conserv
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Best Local Similarity
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
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APPLICANT:
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CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG
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Retter, Mark
Solk, John
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Mitcham, Jennifer L.
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Pred. No. 1.6e-79;
0; Mismatches 0
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                                                            Score 266; DB 4;
Pred. No. 1.8e-79;
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; SOFTWARE: FastSEQ for Wi
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-468
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US-09-439-313-313
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; Sequence 468, Application US/09352616A
; Patent No. 6395278
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Sequence 313, Application US/09439313
PATENT NO. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
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Best Local Similarity
Matches 277; Conserv
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427CB
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ. ID NOS: 472
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APPLICANT: Fanger, ....
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Lay, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILLING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
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US-09-352-616A-313
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Best Local Similarity 98.0
Matches 274; Conservative
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Pred. No. 2.2e-71;
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US-09-352-616A-313
; Sequence 313, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
 APPLICANT: Dillon, Davin C.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Harlocker, Susan Louise
 APPLICANT: Xu, Jiang, Yuqui
 APPLICANT: Xu, Jiangchun
 APPLICANT: Mitcham, Jennifer Lynn
 APPLICANT: Mitcham, Jennifer Lynn
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
 TILE REFERENCE: 210121.427C8
 CURRENT APPLICATION NUMBER: US/09/352,616A
 CURRENT APPLICATION NUMBER: US/09/352,616A
 CURRENT FILING DATE: 1999-07-13
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 313
 LENGTH: 718
 TYPE: DNA
 ORGANISM: Homo sapien

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; LCCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C
US-09-352-616A-313
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
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Best Local Similarity
Matches 274; Conserv
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                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ... (718)
OTHER INFORMATION: n = A,T,C or G
-09-232-149A-313
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                       Match 86.7%;
Local Similarity 98.6%;
the 274; Conservative
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AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                        TCATCGATGAGCCTCGCCCTGTGCCTGNTCCCGCTTGTGAGGGAAAGGACATTAGAAAATG 350
                                                                                                                                                                       TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG 120
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98.6%;
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Sequence 287, Application US/09352616A

Patent No. 6395278

GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Nicoham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIA
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
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                                     US-09-352-616A-287
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SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 287
LENGTH: 301
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                           SOFTWARE: F
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
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                                                   LENGTH: 301
TYPE: DNA
ORGANISM: Homo sapien
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Day, Craig
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Reed, Steven G
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Retter, Mark
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                                                                                                                                  for Windows Version 3.0
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100.0%; Pred. No.
 21.9%;
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. 4.9e-11;
Length 301;
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Query Match

Score 61;

DB 4

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US-09-232-149A-287/c
Sequence 287, Application US/09232149A
Patent No. 6465611
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 287
LENGTH: 301
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ORGANISM: Homo sapien
-09-232-149A-287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-232-463-14/c
COUNTRY: USA
ZIP: 2313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/232,149A CURRENT FILING DATE: 1999-01-15
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OP INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 21.9%; Score 61; DB 4; Length 301; Local Similarity 100.0%; Pred. No. 4.9e-11; nes 61; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                     STREET: 1800 pias
CITY: Alexandria
                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                               DORNER, F
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                                                             US/08/232,463
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                                                                                                                                                                                                                                                                           Suite 500
                                                                                                   Version
                                                                                                   #1.25
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Search completed: February Job time: 53 secs
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US-08-232-463-14
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Best Local :
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                        182 ACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAACA 241
                                                                                                                                                                                                     242 GACGAGAAAATCTTGATGGCTTCACAAG 269
                                                                                                                                                                                                                                                             62 CATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAAGGACATTAGAAAATGA 121
                                                                                                                                                                                                                                                                                                                       N
                                                        RRRRRRRRRRRRRRRRATCGCAAG 1059
                                                                                                                                                                                                                                                                                                                     AGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGGT 61
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   February 1, 2004, 09:50:21 ; Search time 222 Seconds (without alignments) 4563.904 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 1.0
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278
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09A PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09 NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09 NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10B PUBCOMB.seq:*
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6/prodata/2/pubpna/PCTUS PUBCOMB.seq:
6/prodata/2/pubpna/US08 NEW PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ĬĎ.	Description
C :	266	95.7	812	ا و	US-09-759-143-471	Sequence 471, Ag
ი 2	266	95.7	812	9	US-09-780-669-471	471,
α 3	266	95.7	812	ø	US-09-822-827-471	Sequence 471, App
0	266	95.7	812	10	US-09-895-793-471	Sequence 471, 1
ი 5	266	95.7	812	10	US-09-895-814-471	Sequence 471, App
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c 7	266	95.7	812	13	US-10-294-025-471	Sequence 471, 1
ი 8	266	95.7	812	14	US-10-012-896-471	Sequence 471, 1
ი 9	266	95.7	812	15	US-10-010-940-471	Sequence 471, 1
10	266	95.7	876	11	US-09-957-708-3	Sequence 3, App
c 11	266	95.7	2229	9	US-09-759-143-469	Sequence 469, A
c 12	266	95.7	2229	9	US-09-780-669-469	Sequence 469, A
c 13	266	95.7	2229	9	US-09-822-827-469	Sequence 469, Ap
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c 15	266	95.7	2229	-	112-09-895-814-469	Semience 469

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3923	3923	3923	3923	3923	3923	3923	3112	3112	3112	3112	3112	3112	3112	3112	3112	2426	2426	2426	2426	2426	2426	2426	2426	2426	2426	2229	2229	2229	2229
13	13	10	10	9	9	9	15	14	13	13	10	10	9	9	9	15	15	14	13	13	10	10	9	9	φ	15	14	13	Ľ
US-10-294-025-690	US-10-144-678A-690	US-09-895-814-690	US-09-895-793-690	US-09-822-827-690	US-09-780-669-690	US-09-759-143-690	US-10-010-940-468	US-10-012-896-468	US-10-294-025-468	US-10-144-678A-468	US-09-895-814-468	US-09-895-793-468	US-09-822-827-468	US-09-780-669-468	US-09-759-143-468	US-10-205-823-448	US-10-010-940-470	US-10-012-896-470	US-10-294-025-470	US-10-144-678A-470	US-09-895-814-470	US-09-895-793-470	US-09-822-827-470	US-09-780-669-470	US-09-759-143-470	US-10-010-940-469	US-10-012-896-469	US-10-294-025-469	-10
690,	690,	690,	Sequence 690,			690, 1	Sequence 468,	468	468	Sequence 468,	468	e 468	468,	468,	468,	448	470,	470,	470,	470,	470,		470, 1		470,	•	•	Sequence 469,	٠
App	App		App	App	App	App	App	App	App	App	App	App	App				App	App	App	App	App								

ALIGNMENTS

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; TYPE: DNA; ORGANISM: Homo sapiens US-09-759-143-471
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                                                                                                                                       SOFTWARE: F
SEQ ID NO 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Xu, Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 471, Application US/09759143 Patent No. US20020022248A1
 Query Match
Best Local Similarity 99.0
Matches 277; Conservative
                                                                                                                                                                      APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT FILING DATE: 2001-01-12
RUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
RUMBER OF SEQ ID NOS: 934
                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                          LENGTH: 812
                                                                                                                                                                                                                                                                                                                                                                      Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
                                                                                                                                                         FastSEQ for Windows Version 3.0
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Carter, Darrick
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Kalos, Michael
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Mitcham, Jennifer L.
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                  95.7%;
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Score 266; DB: 9;
Pred. No. 9.7e-76;
0; Mismatches 0
                                Length 812;
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Indels

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Gaps

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US-09-780-669-471/c
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                                                                                                                                                      Matches
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                               SOFTWARE: F
SEQ ID NO 471
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: DIAGNOSIS OF
FILE REFERENCE: 210121.427C24
                                                                                                                                                                                                                              LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                              Jocal Similarity 99.6%;
nes 277; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAAGGACATTAGAAAAATG
                                                                                          CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGATCTTTGGG
                                                                                                               CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCCGGCCGCCATCTTGGG
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Carter, Darrick
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Vedvick, Thomas S
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Kalos, Michael D.
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Dillon, Davin C.
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                                                                                                                                                                 Score 266; DB 9;
Pred. No. 9.7e-76;
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                      AND METHODS FOR THE THERAPY AND PROSTATE CANCER
                                                                                                                                                                                    DB 9; Length 812;
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                                                                                                                                                    Indels
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GENERAL INFORMATION:
APPLICANT: XL, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Samuel X.

Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick

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US-09-895-793-471/c
; Sequence 471, Application US/09895793
; Publication No. US20020192763A1
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US-09-822-827-471/c
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GENERAL INFORMATION:

APPLICANT: XU, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICATION UNMEER: US/09/822,827

CURRENT APPLICATION UNMEER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 471

LENGTH: 812

TYPE: NUM
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99.6%;
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Pred. No. 9.7e-76;
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Sequence 471, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
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US-09-895-814-471/c
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; LENGTH: 812
; TYPE: DIA
; ORGANISM: Homo sapiens
US-09-895-793-471
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Best Local (
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SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2001-06-29
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                       Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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                                                                                                          Yasir A.W.
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Pred. No. 9.7e-76;
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; ORGANISM: Homo sapiens
US-09-895-814-471
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APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 471, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local Similarity
Matches 277; Conserv
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APPLICANT: Dillon, Davin C.
APPLICANT: Micham, Jennifer L.
               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
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Vedvick, Thoma.
Carter, Darrick
Li, Samuel X.
Aijun
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Skeiky, Yasir A. W.
Hepler, William T.
Hural, John
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                                                                                            Houghton, Raymond L. Vinals y de Bassols, Foy, Teresa M.
                                                                          Watanabe, Yoshihiro
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10. US20030157089A1
                                                                 Deng, Ta
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ick, Thomas S
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Pred. No. 9.7e-76;
                                                                                                                   Carlota
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; CURRENT FILING DATE: 2002-08-12; NUMBER OF SEQ ID NOS: 1033; SOFTWARE: FastSEQ for Windows Version 3.; SEQ ID NO 471; LENGTH: 812; TYPE: DNA GRGANISM: Homo sapiens
US-10-144-678A-471:
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; ORGANISM: Homo sapiens
US-10-294-025-471
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Best Local S
Matches 277
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CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
RUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
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Matches
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APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                      Docal Similarity 99.6%; les 277; Conservation
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                                               AGACGAGAAATCTTGATGGCTTCACAAGACATGCAAC 286
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Pred. No. 9.7e-76;
0; Mismatches 0;
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Pred. No. 9.7e-76;
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; ORGANISM: Homo sapiens
US-10-012-896-471
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APPLICANT: Xu, Jiangchun
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NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
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Publication No.
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Weagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
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Similarity 99.6%;
77; Conservative
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Mitcham, Jennifer L.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Vedvick, Thomas S.
Carter, Darrick
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Kalos, Michae
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Hepler, William T.
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o. US20020183251A1
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                                                        TTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAAGAAAAC
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Pred. No. 9.7e-76;
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US-10-010-940-471/c; Sequence 471, App; Publication No. U

GENERAL INFORMATION:

Application US/10010940 o. US20030088062A1

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APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Ali, Shujath
TITLE OF INVENTION: Compositions and Methods Relating to
TITLE OF INVENTION: Genes
FILE REFERENCE: DEX-0239
CURRENT APPLICATION NUMBER: US/09/957,708
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/233,746
PRIOR APPLICATION NUMBER: 60/233,746
PRIOR FILING DATE: 2000-09-19
FRIOR FILING DATE: 2000-09-19
FRIOR FILING DATE: 2000-09-19
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US-09-957-708-3
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-940-471
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Best Local Similarity
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APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
NUMBER OF SEQ ID NOS: 575
NUMBER OF SEQ ID NOS: 575
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
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Retter, Mark
Solk, John
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Reed, Steven G.
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99.6%;
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; SEQ ID NO 3
; LENGTH: 876
; TYPE: DNA
; ORCANISM: Homo sapiens
US-09-957-708-3
                                                                                                                    ; SOFTWARE: FastSE
; SEQ ID NO 469
; LENGTH: 2229
; LTYPE: DNA
; ORGANISM: Homo s
US-09-759-143-469
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Best Local Similarity 99.0
Matches 277; Conservative
                                                                         Query Match
Best Local Similarity
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                                                           Matches
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.477C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
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 1617 CAGGAAGCACAAAAGGAAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG
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                 1 CAGGAAGCACAAAAGGAAGCACAGAGATCCCTTGGGAGAAATGCCCCGGCCGCCATCTTGGG
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Carter, Darrick
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Mitcham, Jennifer L.
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                                                            Conservative
                                                                                                                                    sapiens
                                                                         95.7%;
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99.6%;
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                                                       Score 266; DB 9; L
Pred. No. 1.7e-75;
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US-09-780-669-469/c
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CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 277; Conserv
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APPLICANT:
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APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
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AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAAC 240
                                                            TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
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Hepler, William
Hural, John
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Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
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Kalos, Michael D.
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99.6%;
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; ORGANISM: Homo sapiens
US-09-822-827-469
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APPLICANT: X1, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEO ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
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Best Local Similarity
Matches 277; Conserv
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AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 1341
                                                                      AACGGGATTACAGATTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAGGAAAAC 1379
                                                                                                                                             TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCCGCTTGTGAGGGAAGGACATTAGAAAATG
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                              AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 278
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RESULT 14
US-09-895-793-469/c
Sequence 469, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carrer, Darrick
APPLICANT: Carrer, Darrick
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.

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APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: For Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
TYPDE: DNA
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; ORGANISM: Homo sapiens
US-09-895-793-469
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Best Local Similarity
Matches 277; Conservat
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APPLICANT:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
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T: Fanger, Gary R.
INVENTION: COMPOSITIONS AND METHODS FOR THE
INVENTION: DIAGNOSIS OF PROSTATE CANCER
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                    Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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                                                                                                                         Henderson, Robert A.
Hural, John
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Hepler, William T.
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Vedvick, Thomas S.
Carter, Darrick
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                                                     Foy, Teresa
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o. US20020193296A1
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Pred. No. 1.7e-75;
0; Mismatches 0;
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; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
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ALIGNMENTS

MEDLINE PUBMED COMMENT	JOURNAL	TITLE			AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	BF373406	RESULT 1
20202663 10737800 Contact: Simpson A.J.G. Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Ludwig Frof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,	sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Simpson, $A.J.$ Shotgun sequencing of the human transcriptome with ORF expressed	Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and	Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,	1 (bases 1 to 167)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens (human)	EST.	BF373406.1 GI:11335431	BF373406	59-070800-120-H01	BF373406 167 bp mRNA linear EST 24-NOV-2000		

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Email: cgapbs r@mail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqu
Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon,
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 565 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA578773 402 bp mRNA linear EST 12-SEP-199 nh24a04.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:953262, mRNA
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-FT0159-
070800-120-H01&t3=2000-08-07&t4=1)
                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 402)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
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I (bases 1 to 489)

Rocarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., McCarter, M., Clifton, S., Kucaba, T., Theising, B., Bowers, Y., Dante, M., Ritter, E., Bennett, J., Franklin, C., Tesgareishvili, R., Gibbons, M., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
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                                                          The Washington Univ. Nematode EST Project, Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG224987 489 bp mRNA linear EST 09-MP kp52h05.yl TBN95TM-SSFH Strongyloides stercoralis cDNA 5' sin to WP:C08B11.7 CE01477 HYPOTHETICAL 37.7 KD PROTEIN C08B11.7
                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                Unpublished Contact: McCarter JP
                                                                                                                                                                             The Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                                                                                                                                    Panagrolaimoidea;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                            Strongyloides stercoralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strongyloides stercoralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHROMOSOME II ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAACAGACGAGAAAATCTTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTCGACCAGGAAAACAGATCCTGTTGTGGATATATATTTGAACGGGATTACAGATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pAMP10; Site 1: Not1; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
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/note="Vector: pAMP10; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="45 years
/lab_host="DH10B"
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|mol_type="mRNA"
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95.7%;
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Pred. No. 1.9e-22;
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library was constructed

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Thomas Nutman and colleagues

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BX442677/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
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                                                                                                                                                              http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seg=CSODF035AH01NP1&cluster=1534.f. Contact
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                            Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1534.f
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1016)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX442677 Homo sapiens FETAL BRAIN Homo CSODF035YCO1 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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//clone_TVector: Lambda Uni-ZAP XR (Stratagene); Site 1:
//core_Tvector: Lambda Uni-ZAP XR (Stratagene); Site 1:
ECORI, Site 2: XhoI, mRNA was purified from 4 x 1085
filariform Tarvae which had been isolated from infected
humans. cDNA was constructed and, using adaptors, was
cloned unidirectionally into the vector from the ECORI
site to the XhoI site. The library has an unamplified
titer of 1.5 x 10E6 pfu/ml and an amplified, undiluted
titer of 7 x 10E9 pfu/ml. The average insert size of the
unamplifed library is 975 bp (range, 500-1500)."
94 a 47 c 92 g 156 t
                                                                                                                    Avenue Genoscope sequence Location/Qualifiers
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/lab_host="XL-1 Blue MRF' (Stratagene)"
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strain="Filariform larvae obtained from humans"
clone="CS0DF035Y001"
                           db_xref="taxon:9606"
                                                                       organism="Homo sapiens"
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                                               type="mRNA"
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BX436460/c
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                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 GAGCATTACCAATGAGAGGAAAACAGACGAGAAAA 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 GATCCTGTTGTGGATATTTATTTGAACGGGATTACAGATTTGAAATGAAGTCACCAAAGT
  602 KKKAGKAAKAAKAAAADAAAADAAKAKAAGKKKAAAAARKDDKKKKNAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 GTGAGGGAAGGACATTAGAAAATGAATTGATGTTTCCTTAAAGGATGGGCAGGAAAACA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Faraday Avenue Genoscope sequence ID : CSOCAPOOLDF05QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1098)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX436460 Homo sapiens THYMUS 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen.Contact: feng Liang Email: fliang@lifetech.con
http://fulllength.invitrogen.com/ Invitrogen Corporation 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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BP 191 91006 EVRY cedex - France
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                                                                                                    Similarity
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GWGKATKAAAAAATRAKWRAARAARTTRAAADAA 856
                                       GTGAGGGAAGGACATTAGAAAATGAATTGATGTGTTCCTTAAAGGATGGGCAGGAAAACA
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                                                                                     Conservative
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
                                                                                                                                                                                /tissue_type="THYMUS"
/clone_Tib="Homo sapiens THYMUS"
/clone_Tib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
289 c 225 g 229 t 299 others
                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                            clone="CSOCAP001YL10"
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                                                                                                      14.7%;
22.7%;
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                                                                                                      Score 41;
Pred. No.
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137L10 of
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F. Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Estimate of human gene number provided by genome-wide analysis using Tetracdon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
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/mol_type="genomic_DNA"
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High quality sequence stop: 704.
Location/Qualifiers
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Kremizzki, C., Higginbotham, J., Warren, W., Graves, T., Mardis, E.
Gallus gallus BAC End Reads
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Insert Length: 182000 Std Error: (
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Phasianinae; Gallus.
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/strain="Red Jungle Fowl"
/db xref="taxon:9031"
/clone="CH261-96M14"
/sex="female"
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ordering information: http://www.chori.org/bacpac"
a 205 c 203 g 292 t
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                      142 ATGGGCAGGAAAACAGATCCTGTTGTGGATATTTATTTGAACGGGATTACAG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 393)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
                                                                                                                                                             vp28c02.rl Barstead mouse proximal col
clone IMAGE:1077986 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 119 row: I column: 22
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases (v0.980904.e. Vector identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, US
 Marra, M.,
                                                                         Mus musculus
                                                                                                                                                                                                     AA815526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 11 (4), 626-630 (2001)
                                      Mammalia;
                                                      Eukaryota; Metazoa;
                                                                                                                                AA815526.1
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                                                                                         Mus musculus (house
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                   (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
77 c 116 g 87 t 1 others
                 Eutheria;
1 to 206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC_1BOV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Bos taurus"
/mol_type="mRNA"
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Hillier, L., Allen, M., Bowles, M.,
                                                                                                                                GI:2885122
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                                Chordata;
Rodentia;
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Pred. No. 11;
                                                                                                                                                                                    206 bp
e proximal
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                                Sciurognathi;
                                                      Craniata; Vertebrata; Euteleostomi;
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colon MPLRB6 Mus
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Dietrich, N., Dubuque, T.,
                                    Muridae; Murinae; Mus
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                                                                                                                                                                                      musculus
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1 (bases 1 to 384)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 314 200 1017
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone if available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished Contact: Marra M/Mouse EST Project
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                      Mus musculus
                                                                                                                                                             Mus
                                                                                                                                                                             AA710451.1 GI:2720369
EST.
                                                                                                                                                                                                                               vt42f07.rl Barstead mouse proximal colon MPLRB6 clone IMAGE:1165765 5', mRNA sequence.
                                                                                                                                                                                                                                                                  AA710451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                           musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Barstead mouse proximal colon MPLRB6"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site I EcoRI; Site 2: NotI; lst strand cf
was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1077986"
/dev_stage="7 day juvenile"
/lab_host="DH10B"
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strain="FVB/N"
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                                                                                                                                                                                                                                               397 bp mRNA linear UI.M-FOO-cdo-m-15-0-UI.r1 NIH BMAP FOO Mus musculus IMAGE: 6831256 5', mRNA sequence. CA752332 CA752332.1 GI:25582740
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Location/Qualifiers
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; Mu
1 (bases 1 to 397)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                          Mus musculus
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                             Unpublished
                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                            Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="7 day juvenile"
/lab_host="DH10B"
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/clone="IMAGE:1165765"
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56.0%;
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Rodentia;
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Pred. No. 14;
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                                                Plasmodium berghei
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 811)
Carlton,J.M.-R. and Dame,J.B.
The Plasmodium vivax and P. berghei gene sequence tag projective parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
                                                                                                                                                                                                                                                    berghei cDNA 3', mRNA
BF299229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
Parasitol. Today (Regul. Contact: Dame JB
Department of Pathobiolog University of Florida
                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                       BF299229.1 GI:13952844
                                                                                                                                                                                                                                                                                                                             BF299229
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                                                                                                                                                                                            Plasmodium berghei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAACAGACGAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTCTTGGCCAAAATTTAGAAGATGCTGTGAATATCATTTTGAACTTGTGTAAATATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATGAATTGATGTGTTCCTTAA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="embryo 12.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_FOO"

/clone_lib="NIH_BMAP_FOO"

/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;

Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agazose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the NotI site and the polyA tail
is TGAAGAGACC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IMAGE: 6831256"/tissue_type="whole brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6"
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                      Pathobiology, College of Veterinary Medicine
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                                                                                                                                                                                                                                                                               Charles Y sequence.
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Pred. No.
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s Yowell and Jane
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                                                                  ne sequence tag projects
409 (2000)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 TGTCATAAAAATGGGATTGGTCAGACATGGTTGGATAAGACATTCCAAAAAGAAAAGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 GAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATGAATTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 804)

Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                9712 Medical Center Drive, Tel: 301-838-5843
                                                                                                          Unpublished
Other_GSSs: PUGCO69TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUGCO69TB ZM_0.6_1.0_KB Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 ACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGATCTTTGGGTCATCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13(-20)forward
                                                                                  Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                       BZ819014.1 GI:29033836
                                                                                                                                                                                                                                                                                                                                                                                                                               genomic survey sequence
                                                                                                                                                         Maize Genomics Consortium
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301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protocol (J. Carlton et al., manuscript in preparation). PolyA+ RNA was extracted and reverse transcribed using an oligo dT-XhoI primer. Second strand cDNA was prepared using RNase H and DNA polymerase I. EcoR I adaptors were ligated to the cDNA, and it was digested with XhoI. Fragments were size selected, and those between 1-5 kb ligated into EcoRI /XhoI digested vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Pb cDNA #20, Charles Yowell and Jane Carlton"
/note="Vector: pBluescript II vector DNA, excised from
Lamda ZAP II.; Site_1: EcoRI, Site_2: XhoI; Total RNA was
extracted from asynchronous blood stage forms of the
cloned ANKA isolate of P. berghei grown in laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Swiss white mice. Contaminating host white cells had previously been removed using a novel biomagnetic bead protocol (J. Carlton et al., manuscript in preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Plasmodium berghei"
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/lab_host="Swiss white mice"
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dev_stage="asynchron
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Pred. No. 17;
0; Mismatches 65
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Class: sheared ends
                                                                                                                                                                                                                                                              9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
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PUGCO69TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa337L17
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Class: sheared ends.
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                                                                                                                                                                                                                                             Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                 Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                      Other_GSSs: PUGCO69TB
                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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              /db_xref="taxon:4577"
/clone="ZMMBTa337117"
/clone="EMMBTa337117"
/clone="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
a 157 c 158 g 268 t
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/clone_lib="ZM_0.6_1.0_KB"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
141 c 144 g 273 t
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/mol_type="genomic D
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                                                                                                                     /mol_type="genomic DNA"
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Pred. No. 19;
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                                                                                                                                                                                                                                                                                                  Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                      .J., Van Aken,S., Utterback,T., Resnic San Miguel,P., Ma,J. and Bennetzen,J
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Query Match

13.2%;

Score 36.8;

DB 29;

Length 880;

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168 GGATATTTATTTGAACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCA 227

Search completed: February 1, 2004, 10:40:53 Job time : 1319 secs

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
N Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

Ω	C.	ი	ი	ი	ი	ი		Result
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266	266	266	266	266	266	266	278	Score
95.7	95.7	95.7	95.7	95.7	95.7	95.7	100.0	Query Match Length DB ID
812	812	812	812	812	812	812	278	Length
24	22	22	22	22	22	21	22	DB
ABL95270	AAF86949	AAH02871	AAH85120	AAH93806	AAS63899	AAA06690	AAF30667	ID
Human P710P cDNA s	Human P710P invent	Prostate tumour an	Human prostate-spe	Human prostate-spe	Human prostate cDN	Human immunogenic	Human differential	Description

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AAF30666 AAA06545	ACA59834	ABL95397	ABK92196	AAH93861	AAS64026	AAV62430	ACA59704	ABL95267	AAF86946	AAH02868	AAH85117	AAH93803	AAS63896	AAA06687	ACA59706	ABL95269	AAF86948	. AAH02870	AAH85119	AAH93805	AAS63898	AAA06689	ACA59705	ABL95268	AAF86947	AAH02869	AAH85118	AAH93804	AAS63897	AAA06688	AAV62427	AAV62428	ന	AAV62429	ACA59707
Human differential Human immunogenic	Prostate cancer th	Human DD3 cDNA seq	Prostate cancer-as	Gene DD3 cDNA sequ	Human cDNA encodin	Prostate cancer an	Prostate cancer th	Human P710P cDNA s	Human P710P invent	Prostate tumour an	Human prostate-spe	Human prostate-spe	Human prostate cDN	Human immunogenic	Prostate cancer th	Human P710P cDNA s	Human P710P invent	Ου.	Human prostate-spe	Human prostate-spe	Human prostate cDN	Human immunogenic	Prostate cancer th	Human P710P cDNA s	Human P710P invent	Prostate tumour an	Human prostate-spe	Human prostate-spe	Human prostate cDN	Human immunogenic	Prostate cancer an	Prostate cancer an	Human PSNA cDNA, P	Prostate cancer an	Prostate cancer th

ALIGNMENTS

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    29-SEP-1999;
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RESULT 2
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KW Human;
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Best Local S
Matches 278
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                                                                WO200004149-A2
                                                                                                                                                                                                                   Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
                                                                                                                                                                                                                                                                                Human immunogenic
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                                                                                                                             Homo sapiens
                                                                                                                                                                                      immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA06690 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 A; 54 C; 75 G; 59 T; 0 other;
                                                                                                                                                                                                                                                                             prostate tumour protein cDNA sequence SEQ ID NO:471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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27-JAN-2000.

RESULT 3
AAS63899/c
ID AAS638
XX
AC AAS638
AC AAS638
XX
DT 29-JAN
XX
DE Human 1

AAS63899

standard; cDNA; 812

Human prostate cDNA sequence #433

29-JAN-2002 (first entry)

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Best Local :
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14-JUL-1998;
23-SEP-1998;
23-SEP-1998;
23-SEP-1999;
15-JAN-1999;
15-JAN-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used as a probe or comodulate the expression of the polypeptides. AAA06241 to AAA06691 and AAV82000 to AAV82020 represent sequences used in the exemplification of the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 262; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide useful for treating comprises an immunogenic portion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-1999;
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                                                                                                                                              TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
                                                                                AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                                                                                                                                                                                   CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG
AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC
                          AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 278
                                                          AACGGGATTACAGATTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                                                         TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harlocker
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0159812.
98US-0159822.
99US-0232149.
99US-0232880.
99US-0288946.
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98US-0116134
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99.6%;
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                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                             Score 266; DB 21;
Pred. No. 4.7e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and diagnosing prostate cancer prostate tumor protein -
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                                                                                                                                                                                                                                                                                                                                             DB 21;
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286
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Best Local Similarity
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09-MAY-2000; 2000US-0568100.
12-MAY-2000; 2000US-0593793.
13-UUN-2000; 2000US-0605783.
27-JUN-2000; 2000US-0636215.
29-AUG-2000; 2000US-0657279.
06-SEP-2000; 2000US-0657279.
02-OCT-2000; 2000US-0685166.
                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu J,
                                                                                                                                                                                                                                                                                                                                                                     Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 386-387; 579pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2001; 2001WO-US09919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human prostate-specific polypeptides and polynucleotides useful diagnosis and treatment of cancer, especially prostate cancer.
 323
                                                                                         181
                                                                                                                                                      121
                                                                                                                                                                                     502
                                                                                                                                                                                                                                                                                                           277;
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                                                                                                                     TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCCGCTTGTGAGGGAAAGGACATTAGAAAATG
                                                                                                                                                                                                                                                                  CAGGAAGCACAAAAGGAAGCACAGAGATCCCCTGGGAGAAATGCCCCGGCCGCCATCTTGGG
                      AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 278
                                                           AACGGGATTACAGATTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                        PACGGGATTACAGATTTGAPATGAAGTCACCAPAGTGAGCATTACCAPATGAGAGAPAPAC 240
                                                                                                                                                                                                                                             CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG
AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on DC, Mitcham JL, Harlocker SL, Jiang
Retter MW, Stolk JA, Day CH, Vedvick
g A, Skeiky YAW, Hepler WT, Henderson
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                        95.7%;
99.6%;
                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                        Score 266; DB 22;
Pred. No. 4.7e-76;
                                                                                                                                                                                                                                                                                                           0; Indels
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dvick TS,
lerson RA;
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                                                                                                                                                                                                                                                                                                                                        812;
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Carter D;
                                                                                                                                                                                                                                                                                                          1;
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RESULT 4
AAH93806/c
ID AAH938
XX AAH938
XX AAH938
XX AAH938
XX AAH938
XX AAH938
XX O4-OCT
XX Human;
XX Human;
XX Homo: s
PN WO2001
XX U J,
PI Kalos
PI Kalos
PI Kalos
PI Kalos
PI Wang A
XX U J,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (II) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient to cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH9315T to AAH9315T and AAM01115 to AAM01116 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; prostate-specific; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 385; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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MD, Fanger GR,
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                                                                                                                                                                                                          TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGAAAGGACATTAGAAAAATG
                                                                                            TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
                                                                                                                                                                                                                                                                                        CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG
  AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                              95.7%;
99.6%;
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Skeiky
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                                                                                                               Query Match
Best Local Similarity
Matches 277; Conserv
                                                                                                                                                                                             The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG9907 represent polynucleotide and polypeptide sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polypeptide comprising at least prostate-specific protein, useful in the prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate-specific cDNA sequence P710P
                                                                                                                                                                       Sequence 812 BP; 198 A; 189 C; 169 G; 256
                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 284-285; 325pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate specific antigen; PSA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome 22q11.2; prostate-specific protein; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
                                                         562
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                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC, Mitcham JL,
MD, Retter MW, Stolk JA,
                     CAGGAAGCACAAAAGGAAGCACAGAGATCCCCTGGGAGAAATGCCCGGCCGCCCATCTTGGG
                                                                                  CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG
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                                                                                                                Conservative
                                                                                                                             95.7%;
99.6%;
                                                                                                               Score 266; DB 22;
Pred. No. 4.7e-76;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harlocker SL, Jiang Y,
A, Day CH, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                    an immunogenic portion of a diagnosis and therapy of
                                                                                                                                                                        T; 0 other;
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                                                                                                                                          Length 812;
                                                                                                                Indels
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61

1 CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCCGGCCGCCCATCTTGGG

CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG

TCATCGATGAGCCTCGCCCTGTGCCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG

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 Matches
                          Query Match
                                                                             The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I) prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.
                                                        Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                                                   Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-245062/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; prostate tumour antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate tumour antigen cDNA sequence for P710P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
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Local Similarity
nes 277; Conserv
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                                                                                                                                                                                                                                                                                        4; Page 267; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
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 Conservative
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                Score 266; DB 22; Pred. No. 4.7e-76;
                                                                                                                                                                                                                                                                                                                                                                                            Cheever MA;
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cytostatic; vaccine; ss.
Mismatches
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RESULT 7
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                                                                                                                                                         Matches 277;
                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                        The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WTI and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WTI proteins are provided. The human WTI gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a coding sequence used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide comprising part of the Wilm's Tumour gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WTI \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-2001
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                                                                                                                                                                                                                                    Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 220; 228pp; English.
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                                                                                                                                                                            Local Similarity
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                                   TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG 120
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TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
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ilarity 99.6%;
Conservative
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                                                                                                                                                       Score 266; DB 22;
Pred. No. 4.7e-76;
0; Mismatches 0;
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27-JUN-2000; 2000US-0605783.
10-AUG-20000; 2000US-0636215.
29-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0657279.
02-OCT-2000; 2000US-0685166.
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27-MAR-2000;
09-MAY-2000;
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01-AUG-1997;
09-FEB-1998;
25-FEB-1998;
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12-NOV-1999;
18-NOV-1999;
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09-APR-1999;
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23-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cancer; prost
gene therapy; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human P710P cDNA sequence SEQ ID NO 471
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                                                                                       (HARL/)
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(MITC/)
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JIANG Y.

KALOS M D.

KALOS M D.

KANGER G R.

RETTER M W.

STOLK J A.

DAY C H.

VEDVICK T S.

CARTER D.

LI S X.

WANG X.
                                                                                                                 MITCHAM J
                                                                                                        MITCHAM J L.
HARLOCKER S L.
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2000US-0536857.
2000US-0568100.
2000US-0570737.
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gene; ss.
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99US-0439313
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98US-0159812
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Best Local S
Matches 277
                        17-APR-2000;
04-OCT-2000;
28-MAR-2001;
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Fanger
Li SX,
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                                                                                                                                                                                                                                                                                                                                                                                      Prostate cancer therapy associated cDNA #450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 471; 87pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HEND/) HENDERSON
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GR, Retter MW, Stolk JA,
Wang A, Skeiky YAW, Heg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   щ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAAGGACATTAGAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGACGAGAAATCTTGATGGCTTCACAAGACATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention provides prostate-specific coding sequences and ed proteins. These can be used in the diagnosis and treatme particularly prostate cancer. The present sequence is a cl n the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                        2000US-157455P.
2000US-0679272.
2001US-0822827.
                                                                                                             2001US-0895793
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99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 266; DB 24;
Pred. No. 4.7e-76;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Harlocker SL, Jiang Y, JA, Day CH, Vedvick TS, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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                                                                                                                                                                                                                                                                                                                                                fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          812;
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AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC

AACGGGATTACAGATTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAGGAAAAC

324

TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCGCCTTTGGG

TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG

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562

Query Match Best Local Matches

277;

Conservative

0

0

Gaps

Similarity

95.7%; 99.6%;

Score 266; DB 25; Pred. No. 4.7e-76; Mismatches

Length 812; Indels

1 CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCCATCTTGGG

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A PART OF THE PROPERTY OF THE 
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Li SX, Wang ,
Mcneill PD, 1
                                                                       The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated CDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly secrets on effice at
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion protein comprising prostate-specific polypeptides, or its immunogenic portions, useful for diagnosing, preventing and/or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Χu J,
                                                     seqdata.uspto.gov/sequence.html?DocID=US20020192763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-352711/33
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(RETT/)
(STOL/)
(DAYC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (XUJJ/)
(DILL/)
(MITC/)
(HARL/)
(JIAN/)
(KALO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vdedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA, 1 PD, Houghton RL, Y De Bassols CV, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HURAL J.

MCNEILL P D.

HOUGHTON R L.

Y DE BASSOLS
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LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
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DAY C H.
VEDVICK T S.
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MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enic portions, useful for diagonal particularly prostate cancer
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Houghton RL,
BP; 198 A; 189 C; 169
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G; 256
T;
  other;
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Carter D;
Hural J;
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RESULT 10
AAV62429
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                                                                                                                                         Query Match
Best Local S
Matches 277
                                                                                                                                                                                                                                                            of the PCA3 gene. The PCA3 CDNA splice variant 3 sequence, isolated from a human primary prostatic tumour tissue cDNA library, was found in approximately 15% of the cDNA clones isolated. The convention claims for PCA3 CDNA variants and the proteins they encode. The invention also claims for antibodies against PCA3 protein. The antibodies are claimed to be useful for detecting PCA3 protein in convention also claimed to be useful for detecting PCA3 protein in munoassay tests, for diagnosing, assessing and prognosing of immunoassay tests, for diagnosing, assessing and prognosing of corrections pcases and nucleic acids antisense to PCA3 cDNA are claimed to be useful for treating PC, while determining elevated levels of PCA3 (as RNA or protein) is useful for detecting a predisposition to development of PC, e.g. in prenatal tests. Detecting PCA3 protein allows differentiation between malignant and benign prostatic disease, and the level of PCA3 expression allows correlation with the grade of tumour. PCA3 protein and its fragments are also claimed to be useful in vaccines for preventing PC; in drug screens for identifying specific (ant)agonists (potentially useful therapeutically) and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding prostate cancer antigen prevention and treatment of prostatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-568347/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV62429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the prostate cancer antigen (PCA3) cDNA splice variant 3 sequence comprising of exons 1, 3, and 4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Pages 77-78; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prostate cancer antigen (PCA3) cDNA splice variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate cancer antigen cDNA splice variant 3; PCA3; prostatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DIAG-) DIAGNOCURE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
                                                                      256 CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG
                                                                                                       1 CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG
                                                                                                                                                           Similarity
                                                                                                                                                                                                                 820
                      TCATCGATGAGCCTCGCCCTGTGCCCTGGTCCCGCTTGTGAGGGAAAGAGACATTAGAAAATG
                                                                                                                                                                                                                                                  protein-DNA interactions
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TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry
                                                                                                                                                                                                             BP; 262 A; 169 C; 191
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                                                                                                                                                         95.7%;
99.6%;
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                                                                                                                                       Score 266; DB 19;
Pred. No. 4.8e-76;
0; Mismatches 0
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                                                                                                                                                                                                               198 T;
                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                 0 other;
                                                                                                                                                                          Length 820;
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                                                                                                                                       Gaps
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RESULT 11
AAD38815
ID AAD38
XX AAD38
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XX PN WO200
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                                                                                                                                                                                                                      Query Match
Best Local S
Matches 277
                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to prostate specific proteins (PSP) and prostate specific nucleic acids (PSNA). Sequences of the invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating prostate cancer and non-cancerous disease states in prostate. They are also useful for producing engineered prostate tissue for treatment and research. The PSNA sequences are used in gene therapy and for producing transgenic animals and cells. The invention is also used as vaccines. The present sequence is human PSNA cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated prostate specific polypeptide useful for identifying, diagnosing, monitoring, staging, imaging, and treating prostate canc and non-cancerous disease states in prostate -
                                                                                                                                                                                                                                                                                                                                  Sequence 876 BP; 275 A; 183 C; 207 G; 211 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate specific protein; PSP; prostate specific nucleic acid; vaccine; transgenic; prostate cancer; gene therapy; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PSNA cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD38815 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 179; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-471216/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD38815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DIAD-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                      277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.
                                         61 TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
                                                                                                                                                              1 CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCCATCTTGGG
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recipon H, Cafferkey R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIADEXUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
                                                                                                            CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCCGGCCGCCATCTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGACGAGAAATCTTGATGGCTTCACAAGACATGCAAC 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACGGGATTACAGATTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA;
                                                                                                                                                                                                                                                   95.7%;
99.6%;
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                                                                                                                                                                                                                                                   Score 266;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                             CC CDNA splice variant 2 sequence comprising of exons 1, 3, 4a and CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 2 sequence, and CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 2 sequence, CC isolated from a human primary prostatic tumour tissue cDNA library, CC was found in approximately 65% of the cDNA clones isolated. The CC invention claims for PCA3 cDNA variants and the proteins they encode. The invention also claims for antibodies against PCA3 protein. The CC antibodies are claimed to be useful for detecting PCA3 protein in CC immunoassay tests, for diagnosing, assessing and prognosing of communoassay tests, for diagnosing, assessing and prognosing of cc prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed ct be useful for treating PC, while determining elevated levels of CC communoassay tests of communoassay corpotein is useful for detecting a predisposition CC communoassay tests of communoassay tests. Detecting PCA3 protein CC cancer (PC). Autibodies, optionally elevated levels of CC allows differentiation between malignant and benign prostatic disease, CC and the level of PCA3 expression allows correlation with the grade of CC uncour. PCA3 protein and its fragments are also claimed to be useful CC in vaccines for preventing PC; in drug screens for identifying CC spheding profits (potentially useful therapeutically) and for cardoffic canthagonists (potentially useful therapeutically) and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding prostate cancer antigen 3 prevention and treatment of prostatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Pages 76-77; lllpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-568347/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bussemakers MJG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostate cancer antigen (PCA3) cDNA splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV62428 standard; cDNA; 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DIAG-) DIAGNOCURE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                     protein-DNA interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGGGATTACAGATTTGAAATGAAAGTCA-CAAAGTGAGCATTACCAATGAGAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGACGAGAAATCTTGATGGCTTCACAAGACATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0041836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-CA00346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen cDNA splice variant 2; PCA3; prostatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnosis,
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Query Match 95.7 Best Local Similarity 99.6 Matches 277; Conservative

95.7%; 99.6%;

Score 266; DB 19 Pred. No. 7e-76; 0; Mismatches

DB 19; 0

Length 1872; Indels

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Gaps

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Sequence

1872

BP;

567

A; 389 C;

369 G; 539 T; 8

other;

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AAV62427
ID AAV62
XX AAV62
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XX AAV62
XX AAV62
XX AAV62
XX Prost
XX WO984
XX WO984
XX WO984
XX WO984
XX WO984
XX WO984
XX IDAG
XX PPI Busse
XX Prost
XX Prost
XX Track

The present sequence represents the prostate cancer antigen (PCA3) cDNA splice variant I sequence comprising of exons 1, 2, 3, 4a and 4b of the PCA3 gene. The PCA3 CDNA splice variant I sequence, isolated from a human primary prostatic tumour tissue cDNA library, was found in approximately 5% of the cDNA clones isolated. The invention claims for PCA3 cDNA variants and the proteins they encode. The invention also claims for antibodies against PCA3 protein in the antibodies are claimed to be useful for detecting PCA3 protein in immunoassay tests, for diagnosing, assessing and prognosing of
                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding prostate cancer antigen prevention and treatment of prostatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bussemakers MJG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1998;
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                                                                                                                                                                                                                                                                                              Claim 3; Fig 2B-2J; 111pp; English.
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DB; AAW79736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIAGNOCURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
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2019..2024
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 379..534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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RESULT 14
AAA06688/c
ID AAA066
XX AAA066
XX Human
XX Human;
KW Human;
KW immuno
XX Homo s
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Matches 27
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                                                                                          23-SEP-1998;
15-JAN-1999;
15-JAN-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed to be useful for treating PC, while determining elevated levels of PCA3 (as RNA or protein) is useful for detecting a predisposition to development of PC, e.g. in prenatal tests. Detecting PCA3 protein allows differentiation between malignant and benign prostatic disease, and the level of PCA3 expression allows correlation with the grade of tumour. PCA3 protein and its fragments are also claimed to be useful in vaccines for preventing PC, in drug screens for identifying specific (ant)agonists (potentially useful therapeutically) and for studying protein-DNA interactions.
                                                                                                                                                                              14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                     Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
immunogenic; cytostatic; vaccine; ss.
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                               Dillon
                                                                                                                                                                                                                 14-JUL-1999;
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                                                                                                                                                                                                                                                                            WO200004149-A2
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   Human immunogenic prostate tumour protein cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA06688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA06688 standard; cDNA;
   WPI; 2000-171268/15
                                                                                                                                                      23-SEP-1998;
                                                             (CORI-)
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                               Harlocker
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98US-0116134.

98US-0159812.

98US-0159822.

99US-0232149.

99US-0232880.

99US-0288946.
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                               Yuqiu
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Pred. No. 7.3e-76;
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                               Mitcham
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Best Local S
Matches 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides and indicate squainst the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polypucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA06691 and AAV82000 to AAV82020 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2229 BP; 654 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 260-261; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein -
                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 277; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.
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               AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC
                                                                                      AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                                                                                      TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAAGGACATTAGAAAATG
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AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 1341
                                                                 AACGGGATTACAGATTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAGGAAAAC
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                         95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                            447 C; 481 G;
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Pred. No. 7
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                                 278
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RESULT 15
AAS63897/C
ID AAS63897 standard; cDNA; 2229 BP.

XX
AC AAS63897;
XX

CA AAS63897;
XX

DT 29-JAN-2002 (first entry)
XX

DT 29-JAN-2002 (first entry)
XX

Human prostate cDNA sequence #431.
XX

CS Homo sapiens.
XX

OS Homo sapiens.
XX

PN W0200173032-A2.
XX

PN W0200173032-A2.
XX

PF 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0536857.
PR 12-MAY-2000; 2000US-0559793.
PR 13-UN-2000; 2000US-0559793.
PR 13-UN-2000; 2000US-0559793.
PR 13-UN-2000; 2000US-065783.
PR 10-AUG-2000; 2000US-065783.
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Best Local Similarity
Matches 277; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynuclectides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynuclectides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynuclectide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fanger
Li SX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Χu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human prostate-specific polypeptides and polynucleotides useful the diagnosis and treatment of cancer, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-2000; 2000US-0651236.

06-SEP-2000; 2000US-0657279.

02-OCT-2000; 2000US-0679426.

10-OCT-2000; 2000US-0685166.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 385; 579pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated prostate-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639232/73.
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1378
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                                                                                                        AACGGGATTACAGATTTGAAATGAAGTCACCAAAGTGAGCATTACCAATGAGAGAAAAC 240
                                                                                                                                                                TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG 120
                                                                                                                                                                                                                                                                                      CAGGAAGCACAAAAGGAAGCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCATCTTGGG
                                                                                                                                                                                                                                                                                                          CAGGAAGCACAAAAGGAAGCACAGAGAGTCCCTGGGAGAAATGCCCCGGCCGCCCATCTTGGG
                                 AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 278
                                                                                                                                                                                                                 TCATCGATGAGCCTCGCCCTGTGCCTGGTCCCGCTTGTGAGGGAAGGACATTAGAAAATG
                                                                      AACGGGATTACAGATTTGAAATGAAGTCA-CAAAGTGAGCATTACCAATGAGAGGAAAAC 1379
                                                                                                                                             AGACGAGAAAATCTTGATGGCTTCACAAGACATGCAAC 1341
                                                                                                                                                                                                                                                                                                                                                             Conservative
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99.6%;
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Carter D;
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Search completed: February 1, 2004, 09:53:28
Job time : 190 secs